



1/24

SEQUENCE LISTING

<110> Berlin, Vivian
Chiu, Maria Isabel
Cottarel, Guillaume
Damagnez, Veronique

<120> IMMUNOSUPPRESSANT TARGET PROTEINS

<130> APBI-P06-036

<140> US 09/517,491

<141> 2000-03-02

<150> US 08/360,144

<151> 1994-12-20

<150> US 08/250,795

<151> 1994-05-27

<160> 35

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 486

<212> DNA

<213> Mouse

<220>

<221> CDS

<222> (1)...(486)

<400> 1

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Leu	Thr	Arg	His	Asn	Ala	Ala	Asn	Lys	Ile	Leu	Lys	Asn	Met	Cys	Glu	
1				5				10					15			

cac	agc	aac	acg	ctg	gtc	cag	cag	gcc	atg	atg	gtg	agt	gaa	gag	ctg	96
His	Ser	Asn	Thr	Leu	Val	Gln	Gln	Ala	Met	Met	Val	Ser	Glu	Glu	Leu	
			20					25					30			

att	cgg	gta	gcc	atc	ctc	tgg	cat	gag	atg	tgg	cat	gaa	ggc	ctg	gaa	144
Ile	Arg	Val	Ala	Ile	Leu	Trp	His	Glu	Met	Trp	His	Glu	Gly	Leu	Glu	
		35				40					45					

gag	gca	tct	cgc	ttg	tac	ttt	ggg	gag	agg	aac	gtg	aaa	ggc	atg	ttt	192
Glu	Ala	Ser	Arg	Leu	Tyr	Phe	Gly	Glu	Arg	Asn	Val	Lys	Gly	Met	Phe	
	50					55					60					

gag	gtg	ctg	gag	ccc	ctg	cat	gct	atg	atg	gaa	cgg	ggg	ccc	cgg	act	240
Glu	Val	Leu	Glu	Pro	Leu	His	Ala	Met	Met	Glu	Arg	Gly	Pro	Arg	Thr	
	65				70					75					80	

ctg	aag	gaa	aca	tcc	ttt	aat	cag	gca	tat	ggc	cga	gat	tta	atg	gag	288
Leu	Lys	Glu	Thr	Ser	Phe	Asn	Gln	Ala	Tyr	Gly	Arg	Asp	Leu	Met	Glu	
				85					90						95	

gca	caa	gaa	tgg	tgt	cga	aag	tac	atg	aag	tcg	ggg	aac	gtc	aag	gac	336
Ala	Gln	Glu	Trp	Cys	Arg	Lys	Tyr	Met	Lys	Ser	Gly	Asn	Val	Lys	Asp	
		100						105					110			
ctc	acg	caa	gcc	tgg	gac	ctc	tac	tat	cac	gtg	ttc	aga	cgg	atc	tca	384
Leu	Thr	Gln	Ala	Trp	Asp	Leu	Tyr	Tyr	His	Val	Phe	Arg	Arg	Ile	Ser	
		115					120					125				
aag	cag	cta	ccc	cag	ctc	aca	tcc	ctg	gag	ctg	cag	tat	gtg	tcc	ccc	432
Lys	Gln	Leu	Pro	Gln	Leu	Thr	Ser	Leu	Glu	Leu	Gln	Tyr	Val	Ser	Pro	
	130					135					140					
aaa	ctt	ctg	atg	tgc	cga	gac	ctt	gag	ttg	gct	gtg	cca	gga	aca	tac	480
Lys	Leu	Leu	Met	Cys	Arg	Asp	Leu	Glu	Leu	Ala	Val	Pro	Gly	Thr	Tyr	
145					150					155					160	
gac	ccc															486
Asp	Pro															

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 <212> PRT
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<400> 2																	
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His	Ser	Asn	Thr	Leu	Val	Gln	Gln	Ala	Met	Met	Val	Ser	Glu	Glu	Leu		
			20					25					30				
Ile	Arg	Val	Ala	Ile	Leu	Trp	His	Glu	Met	Trp	His	Glu	Gly	Leu	Glu		
		35				40					45						
Glu	Ala	Ser	Arg	Leu	Tyr	Phe	Gly	Glu	Arg	Asn	Val	Lys	Gly	Met	Phe		
	50				55					60							
Glu	Val	Leu	Glu	Pro	Leu	His	Ala	Met	Met	Glu	Arg	Gly	Pro	Arg	Thr		
65				70					75					80			
Leu	Lys	Glu	Thr	Ser	Phe	Asn	Gln	Ala	Tyr	Gly	Arg	Asp	Leu	Met	Glu		
				85				90					95				
Ala	Gln	Glu	Trp	Cys	Arg	Lys	Tyr	Met	Lys	Ser	Gly	Asn	Val	Lys	Asp		
		100					105					110					
Leu	Thr	Gln	Ala	Trp	Asp	Leu	Tyr	Tyr	His	Val	Phe	Arg	Arg	Ile	Ser		
		115				120					125						
Lys	Gln	Leu	Pro	Gln	Leu	Thr	Ser	Leu	Glu	Leu	Gln	Tyr	Val	Ser	Pro		
	130				135						140						
Lys	Leu	Leu	Met	Cys	Arg	Asp	Leu	Glu	Leu	Ala	Val	Pro	Gly	Thr	Tyr		
145				150						155					160		
Asp	Pro																

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<220>
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 <211> 34
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<220>
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<400> 4
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 <211> 348
 <212> DNA
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 <222> (14)...(325)

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 1 5 10

ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg gtg cac tac acc 97
 Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr
 15 20 25

ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc cgt gac cgt aac 145
 Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn
 30 35 40

aag ccc ttt aag ttt atg cta ggc aag cag gag gtg atc cga ggc tgg 193
 Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
 45 50 55 60

gaa gaa ggg gtt gcc cag atg agt gtg ggt cag cgt gcc aaa ctg act 241
 Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
 65 70 75

ata tct cca gat tat gcc tat ggt gcc act ggg cac cca ggc atc atc 289
 Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
 80 85 90

cca cca cat gcc act ctg gtc ttc gat gtg gag ctt ctaaaactgg 335
 Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
 95 100

aatgacggga tcc 348

<210> 6
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
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 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
 20 25 30
 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
 35 40 45
 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
 50 55 60
 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
 65 70 75 80
 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
 85 90 95
 Thr Leu Val Phe Asp Val Glu Leu
 100

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<400> 7
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<210> 8
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<220>
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<400> 8
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 <211> 41
 <212> DNA
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<220>
 <223> oligonucleotide

<400> 9
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<210> 10
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<220>
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<400> 10

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<220>
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 <222> (1)...(5427)

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 1 5 10 15

ctg ggg cac ctg gtc tcc aat gcc ccc cga ctc atc cgc ccc tac atg 96
 Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile Arg Pro Tyr Met
 20 25 30

gag cct att ctg aag gca tta att ttg aaa ctg aaa gat cca gac cct 144
 Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys Asp Pro Asp Pro
 35 40 45

gat cca aac cca ggt gtg atc aat aat gtc ctg gca aca ata gga gaa 192
 Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala Thr Ile Gly Glu
 50 55 60

ttg gca cag gtt agt ggc ctg gaa atg agg aaa tgg gtt gat gaa ctt 240
 Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp Val Asp Glu Leu
 65 70 75 80

ttt att atc atc atg gac atg ctc cag gat tcc tct ttg ttg gcc aaa 288
 Phe Ile Ile Ile Met Asp Met Leu Gln Asp Ser Ser Leu Leu Ala Lys
 85 90 95

agg cag gtg gct ctg tgg acc ctg gga cag ttg gtg gcc agc act ggc 336
 Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val Ala Ser Thr Gly
 100 105 110

tat gta gta gag ccc tac agg aag tac cct act ttg ctt gag gtg cta 384
 Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu Leu Glu Val Leu
 115 120 125

ctg aat ttt ctg aag act gag cag aac cag ggt aca cgc aga gag gcc 432
 Leu Asn Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr Arg Arg Glu Ala
 130 135 140

atc cgt gtg tta ggg ctt tta ggg gct ttg gat cct tac aag cac aaa 480
 Ile Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro Tyr Lys His Lys
 145 150 155 160

gtg aac att ggc atg ata gac cag tcc cgg gat gcc tct gct gtc agc 528
 Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala Ser Ala Val Ser
 165 170 175

ctg tca gaa tcc aag tca agt cag gat tcc tct gac tat agc act agt 576
 Leu Ser Glu Ser Lys Ser Ser Gln Asp Ser Ser Asp Tyr Ser Thr Ser
 180 185 190

gaa atg ctg gtc aac atg gga aac ttg cct ctg gat gag ttc tac cca	624
Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp Glu Phe Tyr Pro	
195 200 205	
gct gtg tcc atg gtg gcc ctg atg cgg atc ttc cga gac cag tca ctc	672
Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg Asp Gln Ser Leu	
210 215 220	
tct cat cat cac acc atg gtt gtc cag gcc atc acc ttc atc ttc aag	720
Ser His His His Thr Met Val Val Gln Ala Ile Thr Phe Ile Phe Lys	
225 230 235 240	
tcc ctg gga ctc aaa tgt gtg cag ttc ctg ccc cag gtc atg ccc acg	768
Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln Val Met Pro Thr	
245 250 255	
ttc ctt aat gtc att cga gtc tgt gat ggg gcc atc cgg gaa ttt ttg	816
Phe Leu Asn Val Ile Arg Val Cys Asp Gly Ala Ile Arg Glu Phe Leu	
260 265 270	
ttc cag cag ctg gga atg ttg gtg tcc ttt gtg aag agc cac atc aga	864
Phe Gln Gln Leu Gly Met Leu Val Ser Phe Val Lys Ser His Ile Arg	
275 280 285	
cct tat atg gat gaa ata gtc acc ctc atg aga gaa ttc tgg gtc atg	912
Pro Tyr Met Asp Glu Ile Val Thr Leu Met Arg Glu Phe Trp Val Met	
290 295 300	
aac acc tca att cag agc acg atc att ctt ctc att gag caa att gtg	960
Asn Thr Ser Ile Gln Ser Thr Ile Ile Leu Leu Ile Glu Gln Ile Val	
305 310 315 320	
gta gct ctt ggg ggt gaa ttt aag ctc tac ctg ccc cag ctg atc cca	1008
Val Ala Leu Gly Gly Glu Phe Lys Leu Tyr Leu Pro Gln Leu Ile Pro	
325 330 335	
cac atg ctg cgt gtc ttc atg cat gac aac agc cca ggc cgc att gtc	1056
His Met Leu Arg Val Phe Met His Asp Asn Ser Pro Gly Arg Ile Val	
340 345 350	
tct atc aag tta ctg gct gca atc cag ctg ttt ggc gcc aac ctg gat	1104
Ser Ile Lys Leu Leu Ala Ala Ile Gln Leu Phe Gly Ala Asn Leu Asp	
355 360 365	
gac tac ctg cat tta ctg ctg cct cct att gtt aag ttg ttt gat gcc	1152
Asp Tyr Leu His Leu Leu Pro Pro Ile Val Lys Leu Phe Asp Ala	
370 375 380	
cct gaa gct cca ctg cca tct cga aag gca gcg cta gag act gtg gac	1200
Pro Glu Ala Pro Leu Pro Ser Arg Lys Ala Ala Leu Glu Thr Val Asp	
385 390 395 400	
cgc ctg acg gag tcc ctg gat ttc act gac tat gcc tcc cgg atc att	1248
Arg Leu Thr Glu Ser Leu Asp Phe Thr Asp Tyr Ala Ser Arg Ile Ile	
405 410 415	

cac cct att gtt cga aca ctg gac cag agc cca gaa ctg cgc tcc aca	1296
His Pro Ile Val Arg Thr Leu Asp Gln Ser Pro Glu Leu Arg Ser Thr	
420 425 430	
gcc atg gac acg ctg tct tca ctt gtt ttt cag ctg ggg aag aag tac	1344
Ala Met Asp Thr Leu Ser Ser Leu Val Phe Gln Leu Gly Lys Lys Tyr	
435 440 445	
caa att ttc att cca atg gtg aat aaa gtt ctg gtg cga cac cga atc	1392
Gln Ile Phe Ile Pro Met Val Asn Lys Val Leu Val Arg His Arg Ile	
450 455 460	
aat cat cag cgc tat gat gtg ctc atc tgc aga att gtc aag gga tac	1440
Asn His Gln Arg Tyr Asp Val Leu Ile Cys Arg Ile Val Lys Gly Tyr	
465 470 475 480	
aca ctt gct gat gaa gag gag gat cct ttg att tac cag cat cgg atg	1488
Thr Leu Ala Asp Glu Glu Glu Asp Pro Leu Ile Tyr Gln His Arg Met	
485 490 495	
ctt agg agt ggc caa ggg gat gca ttg gct agt gga cca gtg gaa aca	1536
Leu Arg Ser Gly Gln Gly Asp Ala Leu Ala Ser Gly Pro Val Glu Thr	
500 505 510	
gga ccc atg aag aaa ctg cac gtc agc acc atc aac ctc caa aag gcc	1584
Gly Pro Met Lys Lys Leu His Val Ser Thr Ile Asn Leu Gln Lys Ala	
515 520 525	
tgg ggc gct gcc agg agg gtc tcc aaa gat gac tgg ctg gaa tgg ctg	1632
Trp Gly Ala Ala Arg Arg Val Ser Lys Asp Asp Trp Leu Glu Trp Leu	
530 535 540	
aga cgg ctg agc ctg gag ctg ctg aag gac tca tca tcg ccc tcc ctg	1680
Arg Arg Leu Ser Leu Glu Leu Leu Lys Asp Ser Ser Ser Pro Ser Leu	
545 550 555 560	
cgc tcc tgc tgg gcc ctg gca cag gcc tac aac ccg atg gcc agg gat	1728
Arg Ser Cys Trp Ala Leu Ala Gln Ala Tyr Asn Pro Met Ala Arg Asp	
565 570 575	
ctc ttc aat gct gca ttt gtg tcc tgc tgg tct gaa ctg aat gaa gat	1776
Leu Phe Asn Ala Ala Phe Val Ser Cys Trp Ser Glu Leu Asn Glu Asp	
580 585 590	
caa cag gat gag ctc atc aga agc atc gag ttg gcc ctc acc tca caa	1824
Gln Gln Asp Glu Leu Ile Arg Ser Ile Glu Leu Ala Leu Thr Ser Gln	
595 600 605	
gac atc gct gaa gtc aca cag acc ctc tta aac ttg gct gaa ttc atg	1872
Asp Ile Ala Glu Val Thr Gln Thr Leu Leu Asn Leu Ala Glu Phe Met	
610 615 620	
gaa cac agt gac aag ggc ccc ctg cca ctg aga gat gac aat ggc att	1920
Glu His Ser Asp Lys Gly Pro Leu Pro Leu Arg Asp Asp Asn Gly Ile	
625 630 635 640	
gtt ctg ctg ggt gag aga gct gcc aag tgc cga gca tat gcc aaa gca	1968
Val Leu Leu Gly Glu Arg Ala Ala Lys Cys Arg Ala Tyr Ala Lys Ala	
645 650 655	

cta cac tac aaa gaa ctg gag ttc cag aaa ggc ccc acc cct gcc att	2016
Leu His Tyr Lys Glu Leu Glu Phe Gln Lys Gly Pro Thr Pro Ala Ile	
660 665 670	
cta gaa tct ctc atc agc att aat aat aag cta cag cag ccg gag gca	2064
Leu Glu Ser Leu Ile Ser Ile Asn Asn Lys Leu Gln Gln Pro Glu Ala	
675 680 685	
gcg gcc gga gtg tta gaa tat gcc atg aaa cac ttt gga gag ctg gag	2112
Ala Ala Gly Val Leu Glu Tyr Ala Met Lys His Phe Gly Glu Leu Glu	
690 695 700	
atc cag gct acc tgg tat gag aaa ctg cac gag tgg gag gat gcc ctt	2160
Ile Gln Ala Thr Trp Tyr Glu Lys Leu His Glu Trp Glu Asp Ala Leu	
705 710 715 720	
gtg gcc tat gac aag aaa atg gac acc aac aag gac gac cca gag ctg	2208
Val Ala Tyr Asp Lys Lys Met Asp Thr Asn Lys Asp Asp Pro Glu Leu	
725 730 735	
atg ctg ggc cgc atg cgc tgc ctc gag gcc ttg ggg gaa tgg ggt caa	2256
Met Leu Gly Arg Met Arg Cys Leu Glu Ala Leu Gly Glu Trp Gly Gln	
740 745 750	
ctc cac cag cag tgc tgt gaa aag tgg acc ctg gtt aat gat gag acc	2304
Leu His Gln Gln Cys Cys Glu Lys Trp Thr Leu Val Asn Asp Glu Thr	
755 760 765	
caa gcc aag atg gcc cgg atg gct gct gca gct gca tgg ggt tta ggt	2352
Gln Ala Lys Met Ala Arg Met Ala Ala Ala Ala Trp Gly Leu Gly	
770 775 780	
cag tgg gac agc atg gaa gaa tac acc tgt atg atc cct cgg gac acc	2400
Gln Trp Asp Ser Met Glu Glu Tyr Thr Cys Met Ile Pro Arg Asp Thr	
785 790 795 800	
cat gat ggg gca ttt tat aga gct gtg ctg gca ctg cat cag gac ctc	2448
His Asp Gly Ala Phe Tyr Arg Ala Val Leu Ala Leu His Gln Asp Leu	
805 810 815	
ttc tcc ttg gca caa cag tgc att gac aag gcc agg gac ctg ctg gat	2496
Phe Ser Leu Ala Gln Gln Cys Ile Asp Lys Ala Arg Asp Leu Leu Asp	
820 825 830	
gct gaa tta act gca atg gca gga gag agt tac agt cgg gca tat ggg	2544
Ala Glu Leu Thr Ala Met Ala Gly Glu Ser Tyr Ser Arg Ala Tyr Gly	
835 840 845	
gcc atg gtt tct tgc cac atg ctg tcc gag ctg gag gag gtt atc cag	2592
Ala Met Val Ser Cys His Met Leu Ser Glu Leu Glu Glu Val Ile Gln	
850 855 860	
tac aaa ctt gtc ccc gag cga cga gag atc atc cgc cag atc tgg tgg	2640
Tyr Lys Leu Val Pro Glu Arg Arg Glu Ile Ile Arg Gln Ile Trp Trp	
865 870 875 880	

gag aga ctg cag ggc tgc cag cgt atc gta gag gac tgg cag aaa atc	2688
Glu Arg Leu Gln Gly Cys Gln Arg Ile Val Glu Asp Trp Gln Lys Ile	
885 890 895	
ctt atg gtg cgg tcc ctt gtg gtc agc cct cat gaa gac atg aga acc	2736
Leu Met Val Arg Ser Leu Val Val Ser Pro His Glu Asp Met Arg Thr	
900 905 910	
tgg ctc aag tat gca agc ctg tgc ggc aag agt ggc agg ctg gct ctt	2784
Trp Leu Lys Tyr Ala Ser Leu Cys Gly Lys Ser Gly Arg Leu Ala Leu	
915 920 925	
gct cat aaa act tta gtg ttg ctc ctg gga gtt gat ccg tct cgg caa	2832
Ala His Lys Thr Leu Val Leu Leu Gly Val Asp Pro Ser Arg Gln	
930 935 940	
ctt gac cat cct ctg cca aca gtt cac cct cag gtg acc tat gcc tac	2880
Leu Asp His Pro Leu Pro Thr Val His Pro Gln Val Thr Tyr Ala Tyr	
945 950 955 960	
atg aaa aac atg tgg aag agt gcc cgc aag atc gat gcc ttc cag cac	2928
Met Lys Asn Met Trp Lys Ser Ala Arg Lys Ile Asp Ala Phe Gln His	
965 970 975	
atg cag cat ttt gtc cag acc atg cag caa cag gcc cag cat gcc atc	2976
Met Gln His Phe Val Gln Thr Met Gln Gln Gln Ala Gln His Ala Ile	
980 985 990	
gct act gag gac cag cag cat aag cag gaa ctg cac aag ctc atg gcc	3024
Ala Thr Glu Asp Gln Gln His Lys Gln Glu Leu His Lys Leu Met Ala	
995 1000 1005	
cga tgc ttc ctg aaa ctt gga gag tgg cag ctg aat cta cag ggc atc	3072
Arg Cys Phe Leu Lys Leu Gly Glu Trp Gln Leu Asn Leu Gln Gly Ile	
1010 1015 1020	
aat gag agc aca atc ccc aaa gtg ctg cag tac tac agc gcc gcc aca	3120
Asn Glu Ser Thr Ile Pro Lys Val Leu Gln Tyr Tyr Ser Ala Ala Thr	
1025 1030 1035 1040	
gag cac gac cgc agc tgg tac aag gcc tgg cat gcg tgg gca gtg atg	3168
Glu His Asp Arg Ser Trp Tyr Lys Ala Trp His Ala Trp Ala Val Met	
1045 1050 1055	
aac ttc gaa gct gtg cta cac tac aaa cat cag aac caa gcc cgc gat	3216
Asn Phe Glu Ala Val Leu His Tyr Lys His Gln Asn Gln Ala Arg Asp	
1060 1065 1070	
gag aag aag aaa ctg cgt cat gcc agc ggg gcc aac atc acc aac gcc	3264
Glu Lys Lys Lys Leu Arg His Ala Ser Gly Ala Asn Ile Thr Asn Ala	
1075 1080 1085	
acc act gcc gcc acc acg gcc gcc act gcc acc acc act gcc agc acc	3312
Thr Thr Ala Ala Thr Thr Ala Ala Thr Ala Thr Thr Ala Ser Thr	
1090 1095 1100	
gag ggc agc aac agt gag agc gag gcc gag agc acc gag aac agc ccc	3360
Glu Gly Ser Asn Ser Glu Ser Glu Ala Glu Ser Thr Glu Asn Ser Pro	
1105 1110 1115 1120	

acc cca tgc ccg ctg cag aag aag gtc act gag gat ctg tcc aaa acc	3408
Thr Pro Ser Pro Leu Gln Lys Lys Val Thr Glu Asp Leu Ser Lys Thr	
1125 1130 1135	
ctc ctg atg tac acg gtg cct gcc gtc cag ggc ttc ttc cgt tcc atc	3456
Leu Leu Met Tyr Thr Val Pro Ala Val Gln Gly Phe Phe Arg Ser Ile	
1140 1145 1150	
tcc ttg tca cga ggc aac aac ctc cag gat aca ctc aga gtt ctc acc	3504
Ser Leu Ser Arg Gly Asn Asn Leu Gln Asp Thr Leu Arg Val Leu Thr	
1155 1160 1165	
tta tgg ttt gat tat ggt cac tgg cca gat gtc aat gag gcc tta gtg	3552
Leu Trp Phe Asp Tyr Gly His Trp Pro Asp Val Asn Glu Ala Leu Val	
1170 1175 1180	
gag ggg gtg aaa gcc atc cag att gat acc tgg cta cag gtt ata cct	3600
Glu Gly Val Lys Ala Ile Gln Ile Asp Thr Trp Leu Gln Val Ile Pro	
1185 1190 1195 1200	
cag ctc att gca aga att gat acg ccc aga ccc ttg gtg gga cgt ctc	3648
Gln Leu Ile Ala Arg Ile Asp Thr Pro Arg Pro Leu Val Gly Arg Leu	
1205 1210 1215	
att cac cag ctt ctc aca gac att ggt cgg tac cac ccc cag gcc ctc	3696
Ile His Gln Leu Leu Thr Asp Ile Gly Arg Tyr His Pro Gln Ala Leu	
1220 1225 1230	
atc tac cca ctg aca gtg gct tct aag tct acc acg aca gcc cgg cac	3744
Ile Tyr Pro Leu Thr Val Ala Ser Lys Ser Thr Thr Thr Ala Arg His	
1235 1240 1245	
aat gca gcc aac aag att ctg aag aac atg tgt gag cac agc aac acc	3792
Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu His Ser Asn Thr	
1250 1255 1260	
ctg gtc cag cag gcc atg atg gtg agc gag gag ctg atc cga gtg gcc	3840
Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu Ile Arg Val Ala	
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atc ctc tgg cat gag atg tgg cat gaa ggc ctg gaa gag gca tct cgt	3888
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Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu	
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ccc ttg cat gct atg atg gaa cgg ggc ccc cag act ctg aag gaa aca	3984
Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr	
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Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp	
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tgc Cys 1345	agg Arg	aag Lys	tac Tyr	atg Met	aaa Lys 1350	tca Ser	ggg Gly	aat Asn	gtc Val	aag Lys 1355	gac Asp	ctc Leu	acc Thr	caa Gln	gcc Ala 1360	4080
tgg Trp	gac Asp	ctc Leu	tat Tyr	tat Tyr 1365	cat His	gtg Val	ttc Phe	cga Arg	cga Arg 1370	atc Ile	tca Ser	aag Lys	cag Gln	ctg Leu 1375	cct Pro	4128
cag Gln	ctc Leu	aca Thr	tcc Ser 1380	tta Leu	gag Glu	ctg Leu	caa Gln	tat Tyr 1385	gtt Val	tcc Ser	cca Pro	aaa Lys	ctt Leu 1390	ctg Leu	atg Met	4176
tgc Cys	cgg Arg	gac Asp 1395	ctt Leu	gaa Glu	ttg Leu	gct Ala	gtg Val 1400	cca Pro	gga Gly	aca Thr	tat Tyr	gac Asp 1405	ccc Pro	aac Asn	cag Gln	4224
cca Pro	atc Ile 1410	att Ile	cgc Arg	att Ile	cag Gln	tcc Ser 1415	ata Ile	gca Ala	ccg Pro	tct Ser	ttg Leu 1420	caa Gln	gtc Val	atc Ile	aca Thr	4272
tcc Ser 1425	aag Lys	cag Gln	agg Arg	ccc Pro	cgg Arg 1430	aaa Lys	ttg Leu	aca Thr	ctt Leu	atg Met 1435	ggc Gly	agc Ser	aac Asn	gga Gly	cat His 1440	4320
gag Glu	ttt Phe	gtt Val	ttc Phe 1445	ctt Leu	cta Leu	aaa Lys	ggc Gly	cat His	gaa Glu 1450	gat Asp	ctg Leu	cgc Arg	cag Gln	gat Asp 1455	gag Glu	4368
cgt Arg	gtg Val	atg Met	cag Gln 1460	ctc Leu	ttc Phe	ggc Gly	ctg Leu	gtt Val 1465	aac Asn	acc Thr	ctt Leu	ctg Leu	gcc Ala 1470	aat Asn	gac Asp	4416
cca Pro	aca Thr	tct Ser 1475	ctt Leu	cgg Arg	aaa Lys	aac Asn	ctc Leu 1480	agc Ser	atc Ile	cag Gln	aga Arg	tac Tyr 1485	gct Ala	gtc Val	atc Ile	4464
cct Pro 1490	tta Leu	tcg Ser	acc Thr	aac Asn	tcg Ser	ggc Gly 1495	ctc Leu	att Ile	ggc Gly	tgg Trp	gtt Val 1500	ccc Pro	cac His	tgt Cys	gac Asp	4512
aca Thr 1505	ctg Leu	cac His	gcc Ala	ctc Leu	atc Ile 1510	cgg Arg	gac Asp	tac Tyr	agg Arg	gag Glu 1515	aag Lys	aag Lys	aag Lys	atc Ile	ctt Leu 1520	4560
ctc Leu	aac Asn	atc Ile	gag Glu 1525	cat His	cgc Arg	atc Ile	atg Met	ttg Leu	cgg Arg 1530	atg Met	gct Ala	ccg Pro	gac Asp	tat Tyr 1535	gac Asp	4608
cac His	ttg Leu	act Thr	ctg Leu 1540	atg Met	cag Gln	aag Lys	gtg Val	gag Glu 1545	gtg Val	ttt Phe	gag Glu	cat His	gcc Ala 1550	gtc Val	aat Asn	4656
aat Asn	aca Thr	gct Ala 1555	ggg Gly	gac Asp	gac Asp	ctg Leu	gcc Ala 1560	aag Lys	ctg Leu	ctg Leu	tgg Trp	ctg Leu	aaa Lys	agc Ser	ccc Pro	4704
agc Ser	tcc Ser 1570	gag Glu	gtg Val	tgg Trp	ttt Phe 1575	gac Asp	cga Arg 1580	aga Arg	acc Thr	aat Asn	tat Tyr 1580	acc Thr	cgt Arg	tct Ser	tta Leu	4752

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Pro Ser Asn Leu Met Leu Asp Arg Leu Ser Gly Lys Ile Leu His Ile	
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Asp Phe Gly Asp Cys Phe Glu Val Ala Met Thr Arg Glu Lys Phe Pro	
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Glu Lys Ile Pro Phe Arg Leu Thr Arg Met Leu Thr Asn Ala Met Glu	
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Val Thr Gly Leu Asp Gly Asn Tyr Arg Ile Thr Cys His Thr Val Met	
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Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala Val Leu Glu Ala	
1665 1670 1675 1680	
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Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met Asp Thr Asn Thr	
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aaa ggc aac aag cga tcc cga acg agg acg gat tcc tac tct gct ggc	5136
Lys Gly Asn Lys Arg Ser Arg Thr Arg Thr Asp Ser Tyr Ser Ala Gly	
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Gln Ser Val Glu Ile Leu Asp Gly Val Glu Leu Gly Glu Pro Ala His	
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Lys Lys Thr Gly Thr Thr Val Pro Glu Ser Ile His Ser Phe Ile Gly	
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Asp Gly Leu Val Lys Pro Glu Ala Leu Asn Lys Lys Ala Ile Gln Ile	
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att aac agg gtt cga gat aag ctc act ggt cgg gac ttc tct cat gat	5328
Ile Asn Arg Val Arg Asp Lys Leu Thr Gly Arg Asp Phe Ser His Asp	
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Asp Thr Leu Asp Val Pro Thr Gln Val Glu Leu Leu Ile Lys Gln Ala	
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Trp	

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 35 40 45
 Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala Thr Ile Gly Glu
 50 55 60
 Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp Val Asp Glu Leu
 65 70 75 80
 Phe Ile Ile Ile Met Asp Met Leu Gln Asp Ser Ser Leu Leu Ala Lys
 85 90 95
 Arg Gln Val Ala Leu Trp Thr Leu Gly Gln Leu Val Ala Ser Thr Gly
 100 105 110
 Tyr Val Val Glu Pro Tyr Arg Lys Tyr Pro Thr Leu Leu Glu Val Leu
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 Leu Asn Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr Arg Arg Glu Ala
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 Ile Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro Tyr Lys His Lys
 145 150 155 160
 Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala Ser Ala Val Ser
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 Leu Ser Glu Ser Lys Ser Ser Gln Asp Ser Ser Asp Tyr Ser Thr Ser
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 Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp Glu Phe Tyr Pro
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 Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg Asp Gln Ser Leu
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 Ser His His His Thr Met Val Val Gln Ala Ile Thr Phe Ile Phe Lys
 225 230 235 240
 Ser Leu Gly Leu Lys Cys Val Gln Phe Leu Pro Gln Val Met Pro Thr
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 Phe Leu Asn Val Ile Arg Val Cys Asp Gly Ala Ile Arg Glu Phe Leu
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 Phe Gln Gln Leu Gly Met Leu Val Ser Phe Val Lys Ser His Ile Arg
 275 280 285
 Pro Tyr Met Asp Glu Ile Val Thr Leu Met Arg Glu Phe Trp Val Met
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 Asn Thr Ser Ile Gln Ser Thr Ile Ile Leu Leu Ile Glu Gln Ile Val
 305 310 315 320
 Val Ala Leu Gly Gly Glu Phe Lys Leu Tyr Leu Pro Gln Leu Ile Pro
 325 330 335
 His Met Leu Arg Val Phe Met His Asp Asn Ser Pro Gly Arg Ile Val
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 Ser Ile Lys Leu Leu Ala Ala Ile Gln Leu Phe Gly Ala Asn Leu Asp
 355 360 365
 Asp Tyr Leu His Leu Leu Leu Pro Pro Ile Val Lys Leu Phe Asp Ala
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 Pro Glu Ala Pro Leu Pro Ser Arg Lys Ala Ala Leu Glu Thr Val Asp
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His	Pro	Ile	Val	Arg	Thr	Leu	Asp	Gln	Ser	Pro	Glu	Leu	Arg	Ser	Thr
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Ala	Met	Asp	Thr	Leu	Ser	Ser	Leu	Val	Phe	Gln	Leu	Gly	Lys	Lys	Tyr
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Trp	Gly	Ala	Ala	Arg	Arg	Val	Ser	Lys	Asp	Asp	Trp	Leu	Glu	Trp	Leu
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Asp	Ile	Ala	Glu	Val	Thr	Gln	Thr	Leu	Leu	Asn	Leu	Ala	Glu	Phe	Met
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Glu	His	Ser	Asp	Lys	Gly	Pro	Leu	Pro	Leu	Arg	Asp	Asp	Asn	Gly	Ile
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Val	Leu	Leu	Gly	Glu	Arg	Ala	Ala	Lys	Cys	Arg	Ala	Tyr	Ala	Lys	Ala
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Leu	His	Tyr	Lys	Glu	Leu	Glu	Phe	Gln	Lys	Gly	Pro	Thr	Pro	Ala	Ile
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Leu	Glu	Ser	Leu	Ile	Ser	Ile	Asn	Asn	Lys	Leu	Gln	Gln	Pro	Glu	Ala
		675					680					685			
Ala	Ala	Gly	Val	Leu	Glu	Tyr	Ala	Met	Lys	His	Phe	Gly	Glu	Leu	Glu
	690					695					700				
Ile	Gln	Ala	Thr	Trp	Tyr	Glu	Lys	Leu	His	Glu	Trp	Glu	Asp	Ala	Leu
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Val	Ala	Tyr	Asp	Lys	Lys	Met	Asp	Thr	Asn	Lys	Asp	Asp	Pro	Glu	Leu
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Met	Leu	Gly	Arg	Met	Arg	Cys	Leu	Glu	Ala	Leu	Gly	Glu	Trp	Gly	Gln
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Leu	His	Gln	Gln	Cys	Cys	Glu	Lys	Trp	Thr	Leu	Val	Asn	Asp	Glu	Thr
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Gln	Ala	Lys	Met	Ala	Arg	Met	Ala	Ala	Ala	Ala	Ala	Trp	Gly	Leu	Gly
	770					775						780			
Gln	Trp	Asp	Ser	Met	Glu	Glu	Tyr	Thr	Cys	Met	Ile	Pro	Arg	Asp	Thr
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His	Asp	Gly	Ala	Phe	Tyr	Arg	Ala	Val	Leu	Ala	Leu	His	Gln	Asp	Leu
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Phe	Ser	Leu	Ala	Gln	Gln	Cys	Ile	Asp	Lys	Ala	Arg	Asp	Leu	Leu	Asp
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Ala	Glu	Leu	Thr	Ala	Met	Ala	Gly	Glu	Ser	Tyr	Ser	Arg	Ala	Tyr	Gly
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Ala	Met	Val	Ser	Cys	His	Met	Leu	Ser	Glu	Leu	Glu	Glu	Val	Ile	Gln
	850					855						860			

Tyr	Lys	Leu	Val	Pro	Glu	Arg	Arg	Glu	Ile	Ile	Arg	Gln	Ile	Trp	Trp	865	870	875	880
Glu	Arg	Leu	Gln	Gly	Cys	Gln	Arg	Ile	Val	Glu	Asp	Trp	Gln	Lys	Ile				
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Trp	Leu	Lys	Tyr	Ala	Ser	Leu	Cys	Gly	Lys	Ser	Gly	Arg	Leu	Ala	Leu				
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Ala	Thr	Glu	Asp	Gln	Gln	His	Lys	Gln	Glu	Leu	His	Lys	Leu	Met	Ala				
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 Pro Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu Gln Val Ile Thr
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 Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly Ser Asn Gly His
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 aatgaattgg aaataagaaa cgctagagct gcattagtgt tgaaacgtat taccgataag 1560
 ttaactggta acgatatcaa acggttgaga ggattagatg tgcctactca agtcgataaa 1620
 ttgattcaac aagccaccag tgttgagaat ttgtgtcagc attacattgg ttggtgttcg 1680
 tgttggtagg ttgattatcg tcatgtgtcg ataagtatgg tattgtggta actattttat 1740
 aaagggaaat attaaagaat tgtatattat taaaaaaaaa aaaaaaaact cgag 1794

<210> 14
 <211> 562
 <212> PRT
 <213> C. albicans

<400> 14
 Leu Val Tyr Pro Leu Thr Val Ala Ile Thr Ser Glu Ser Thr Ser Arg
 1 5 10 15
 Lys Lys Ala Ala Gln Ser Ile Ile Glu Lys Met Arg Val His Ser Pro
 20 25 30
 Ser Leu Val Asp Gln Ala Glu Leu Val Ser Arg Glu Leu Ile Arg Val
 35 40 45
 Ala Val Leu Trp His Glu Gln Trp His Asp Ala Leu Glu Asp Ala Ser
 50 55 60
 Arg Phe Phe Phe Gly Glu His Asn Thr Glu Lys Met Phe Glu Thr Leu
 65 70 75 80

Glu	Pro	Leu	His	Gln	Met	Leu	Gln	Lys	Gly	Pro	Glu	Thr	Met	Arg	Glu
			85						90					95	
Gln	Ala	Phe	Ala	Asn	Ala	Phe	Gly	Arg	Glu	Leu	Thr	Asp	Ala	Tyr	Glu
		100					105						110		
Trp	Val	Leu	Asn	Phe	Arg	Arg	Thr	Lys	Asp	Ile	Thr	Asn	Leu	Asn	Gln
	115						120					125			
Ala	Trp	Asp	Ile	Tyr	Tyr	Asn	Val	Phe	Arg	Arg	Val	Ser	Lys	Gln	Val
	130					135					140				
Gln	Leu	Leu	Ala	Ser	Leu	Glu	Leu	Gln	Tyr	Val	Ser	Pro	Asp	Leu	Glu
145					150					155					160
His	Ala	Gln	Asp	Leu	Glu	Leu	Ala	Val	Pro	Gly	Thr	Tyr	Gln	Ala	Gly
			165						170					175	
Lys	Pro	Val	Ile	Arg	Ile	Ile	Lys	Phe	Asp	Pro	Thr	Phe	Ser	Ile	Ile
		180						185					190		
Ser	Ser	Lys	Gln	Arg	Pro	Arg	Lys	Leu	Ser	Cys	Arg	Gly	Ser	Asp	Gly
		195					200					205			
Lys	Asp	Tyr	Gln	Tyr	Ala	Leu	Lys	Gly	His	Glu	Asp	Ile	Arg	Gln	Asp
	210					215					220				
Asn	Leu	Val	Met	Gln	Leu	Phe	Gly	Leu	Val	Asn	Thr	Leu	Leu	Val	Asn
225					230					235					240
Asp	Pro	Val	Cys	Phe	Lys	Arg	His	Leu	Asp	Ile	Gln	Gln	Tyr	Pro	Ala
			245						250					255	
Ile	Pro	Leu	Ser	Pro	Lys	Val	Gly	Leu	Leu	Gly	Trp	Val	Pro	Asn	Ser
		260						265					270		
Asp	Thr	Phe	His	Val	Leu	Ile	Lys	Gly	Tyr	Arg	Glu	Ser	Arg	Ser	Ile
	275						280					285			
Met	Leu	Asn	Ile	Glu	His	Arg	Leu	Leu	Leu	Gln	Met	Ala	Pro	Asp	Tyr
	290					295					300				
Asp	Phe	Leu	Thr	Leu	Leu	Gln	Lys	Val	Glu	Val	Phe	Thr	Ser	Ala	Met
305					310					315					320
Asp	Asn	Cys	Lys	Gly	Gln	Asp	Leu	Tyr	Lys	Val	Leu	Trp	Leu	Lys	Ser
			325						330					335	
Lys	Ser	Ser	Glu	Ala	Trp	Leu	Asp	Arg	Arg	Thr	Thr	Tyr	Thr	Arg	Ser
		340					345						350		
Leu	Ala	Val	Met	Ser	Met	Val	Gly	Tyr	Ile	Leu	Gly	Leu	Gly	Asp	Arg
	355						360					365			
His	Pro	Ser	Asn	Leu	Met	Leu	Asp	Arg	Ile	Thr	Gly	Lys	Val	Ile	His
	370					375					380				
Ile	Asp	Phe	Gly	Asp	Cys	Phe	Glu	Ala	Ala	Ile	Leu	Arg	Glu	Lys	Tyr
385					390					395					400
Pro	Glu	Arg	Val	Pro	Phe	Arg	Leu	Thr	Arg	Met	Leu	Asn	Tyr	Ala	Met
			405						410					415	
Glu	Val	Ser	Gly	Ile	Glu	Gly	Ser	Phe	Arg	Ile	Thr	Cys	Glu	His	Val
		420						425					430		
Met	Arg	Val	Leu	Arg	Asp	Asn	Lys	Glu	Ser	Leu	Met	Ala	Ile	Leu	Glu
	435						440					445			
Ala	Phe	Ala	Tyr	Asp	Pro	Leu	Ile	Asn	Trp	Gly	Phe	Asp	Phe	Pro	Thr
	450					455					460				
Lys	Ala	Leu	Ala	Glu	Ser	Thr	Gly	Ile	Arg	Val	Pro	Gln	Val	Asn	Thr
465					470					475					480
Ala	Glu	Leu	Leu	Arg	Arg	Gly	Gln	Ile	Asp	Glu	Lys	Glu	Ala	Val	Arg
			485						490					495	
Leu	Gln	Lys	Gln	Asn	Glu	Leu	Glu	Ile	Arg	Asn	Ala	Arg	Ala	Ala	Leu
		500						505					510		
Val	Leu	Lys	Arg	Ile	Thr	Asp	Lys	Leu	Thr	Gly	Asn	Asp	Ile	Lys	Arg
	515						520					525			
Leu	Arg	Gly	Leu	Asp	Val	Pro	Thr	Gln	Val	Asp	Lys	Leu	Ile	Gln	Gln
	530					535					540				

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Ala Thr Ser Val Glu Asn Leu Cys Gln His Tyr Ile Gly Trp Cys Ser
545 550 555 560
Cys Trp

<210> 15
<211> 399
<212> DNA
<213> Homo sapiens

<400> 15
gttagtcacg agttgatcag agtagccggt ctatggcacg aattatggta tgaaggactg 60
gaagatgcga gccgccaatt tttcgttgaa cataacatag aaaaaatggt ttctacttta 120
gaacctttac ataaacactt aggcaatgag cctcaaactg taagtgaggt atcgtttcag 180
aaatcatttg gtagagattt gaacgatgcc tacgaatggt tgaataacta caaaaagtca 240
aaagacatca ataatttgaa ccaagcttgg gatattttatt ataacgtctt cagaaaaata 300
acacgtcaaa taccacagtt acaaacctta gacttacagc atgtttctcc ccagcttctg 360
gctactcatg atctcgaatt ggctgttcct gggacatat 399

<210> 16
<211> 133
<212> PRT
<213> Homo sapiens

<400> 16
Val Ser His Glu Leu Ile Arg Val Ala Val Leu Trp His Glu Leu Trp
1 5 10 15
Tyr Glu Gly Leu Glu Asp Ala Ser Arg Gln Phe Phe Val Glu His Asn
20 25 30
Ile Glu Lys Met Phe Ser Thr Leu Glu Pro Leu His Lys His Leu Gly
35 40 45
Asn Glu Pro Gln Thr Leu Ser Glu Val Ser Phe Gln Lys Ser Phe Gly
50 55 60
Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Asn Asn Tyr Lys Lys Ser
65 70 75 80
Lys Asp Ile Asn Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val
85 90 95
Phe Arg Lys Ile Thr Arg Gln Ile Pro Gln Leu Gln Thr Leu Asp Leu
100 105 110
Gln His Val Ser Pro Gln Leu Leu Ala Thr His Asp Leu Glu Leu Ala
115 120 125
Val Pro Gly Thr Tyr
130

<210> 17
<211> 399
<212> DNA
<213> Homo sapiens

<400> 17
gtcagccacg aattgatacg tatggcggtg ctttggcatg agcaatggta tgagggtctg 60
gatgacgccg gtaggcagtt ttttgagaga cataataccg aaaaaatggt tgctgcttta 120
gagcctctgt acgaaatgct gaagagagga ccggaaactt tgagggaaat atcgttccaa 180
aattcttttg gtagggactt gaatgacgct tacgaatggc tgatgaatta caaaaaatct 240
aaagatgtta gtaatttaaa ccaagcgtgg gacattttact ataatgtttt caggaaaatt 300
ggtaaacagt tgccacaatt acaaactctt gaactacaac atgtgtcgcc aaaactacta 360
tctgcgcgat atttggaatt ggctgtcccc gggacccgt 399

<210> 18
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 18
 Val Ser His Glu Leu Ile Arg Met Ala Val Leu Trp His Glu Gln Trp
 1 5 10 15
 Tyr Glu Gly Leu Asp Asp Ala Ser Arg Gln Phe Phe Gly Glu His Asn
 20 25 30
 Thr Glu Lys Met Phe Ala Ala Leu Glu Pro Leu Tyr Glu Met Leu Lys
 35 40 45
 Arg Gly Pro Glu Thr Leu Arg Glu Ile Ser Phe Gln Asn Ser Phe Gly
 50 55 60
 Arg Asp Leu Asn Asp Ala Tyr Glu Trp Leu Met Asn Tyr Lys Lys Ser
 65 70 75 80
 Lys Asp Val Ser Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val
 85 90 95
 Phe Arg Lys Ile Gly Lys Gln Leu Pro Gln Leu Gln Thr Leu Glu Leu
 100 105 110
 Gln His Val Ser Pro Lys Leu Leu Ser Ala His Asp Leu Glu Leu Ala
 115 120 125
 Val Pro Gly Thr Arg
 130

<210> 19
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 59, 64, 72, 74, 89, 94, 101, 137, 158, 175, 190, 201, 207,
 210, 213, 218, 234, 243, 257, 283, 286, 289, 292, 314, 325,
 328, 335, 352, 361, 380, 384, 390, 393, 403, 411, 413, 427,
 432, 435, 440, 443, 450, 452, 460, 465, 480, 482, 486
 <223> n = A,T,C or G

<221> misc_feature
 <222> 492, 515
 <223> n = A,T,C or G

<400> 19
 tgaccctcac cccttccacc tatcccaaaa acctcactgg gtctgtggac aaacaacana 60
 aatnttttcc ananaggccc caaatgagnc ccanggggtct ntcttccatc agacccagtg 120
 attctgcgac tcacacnctt caattcaaga cctgaccnct agtagggagg ttantcaga 180
 tcgctggcan cctcggtga ncagatncan agnggggntc gctgttcagt gggncacccc 240
 tcnctggcct tcttcancag ggggtctggga tgttttcagt ggncnaana cnctgtttag 300
 agccagggct cagnaaacag aaaanctntc atggngggttc tggacacagg gnagggtctgg 360
 nacatattgg ggattatgan cagnaccaan acnccactaa atnccccaag nanaaagtg 420
 aaccatntct anacnccatn ttntatcagn anaaattttn ttccnataaa tgacatcagn 480
 antttnaaca tnaaaaaaaaa aaaaaaaaaa aaaaanaaaaa aaaaaaaaaa a 531

<210> 20
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 20
gcgtataacg cgtttgggaat cactacaggg atgtttaata ccactacaat ggatgatgta 60
tataactatc tattcgatga tgaagatacc ccaccaaacc caaaaaaaga gatctggaat 120
tcggatcctc gagagatcta tgaatcgtag atactgaaaa accccgcaag ttcacttcaa 180
ctgtgcatcg tgcaccatct caatttcttt catttataca tcgttttgcc t 231

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 21
tgaagatacc ccaccaaacc c 21

<210> 22
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 22
tgcacagttg aagtgaac 18

<210> 23
<211> 662
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 27, 373, 443, 461, 483, 485, 507, 583, 588, 593, 605, 606,
607, 612, 624, 625, 626, 627, 628, 630, 631, 632, 635, 639,
646, 652, 659, 661
<223> n = A,T,C or G

<400> 23
accaaaccga aaaaaagaga tcctagnaac tagtggatcc cccgggctgc aggaattcgg 60
tacgagtcgc cctcagcaga ctgcgccagg agaggaaagc atggaggaaa gaccacccat 120
ttggtttcgt ggctgtccca acaaaaaatc ccgatggcac gatgaacctc atgaactggg 180
agtgcgccat tccaggaaag aaagggactc cgtgggaagg aggcttggtt aaactacgga 240
tgcttttcaa agatgattat ccattcttcgc caccaaaatg taaattcgaa ccaccattat 300
ttcacccgaa tgtgtaccct tcggggacag tgtgcctgtc catcttagag gaggacaagg 360
actggagggc agncatcaca atcaaacagg atcctattag gaatacagga actttctaaa 420
tgaaccaa atccaagacc agntcaagca gagggctaca ngatttactg ccaaaacaga 480
gtngngtacg agaaagggtc cgagcanagc cagaagtttg ggcctcatta gcaggacact 540
gggtggatcgt caaaggaggt ttggttgagg agacttggtc aanatttngg aanttaagtt 600
gtccnnaaac tngcgggggg gggnnnnn nnttnccant tccctncccc cngtthttng 660
nt 662

<210> 24
<211> 119
<212> PRT
<213> Homo sapiens

<220>

<221> VARIANT

<222> 105

<223> Xaa = Any Amino Acid

<400> 24

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Val Arg Val Ala Leu Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp Arg
 1           5           10           15
Lys Asp His Pro Phe Gly Phe Val Ala Val Pro Thr Lys Asn Pro Asp
           20           25           30
Gly Thr Met Asn Leu Met Asn Trp Glu Cys Ala Ile Pro Gly Lys Lys
           35           40           45
Gly Thr Pro Trp Glu Gly Gly Leu Phe Lys Leu Arg Met Leu Phe Lys
           50           55           60
Asp Asp Tyr Pro Ser Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro Leu
65           70           75           80
Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile Leu
           85           90           95
Glu Glu Asp Lys Asp Trp Arg Ala Xaa Ile Thr Ile Lys Gln Asp Pro
           100          105          110
Ile Arg Asn Thr Gly Thr Phe
           115

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<210> 25

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<221> misc_feature

<222> 112, 148, 158, 171, 178, 182, 191, 194, 203, 204

<223> n = A,T,C or G

<400> 25

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ccctccctcc tgccgctcct ctctagaacc ttctagaacc tgggctgtgc tgcttttgag 60
cctcagaccc cagggcagca tctcggttct gcgccacttc ctttgtgttt anatggcggt 120
ttgtctgtgt tgctgtttag agtagatnaa ctgtttanat aaaaaaaaaa naaaattnac 180
tngagggggc ntgnaggcat gcnaac 207

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<210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 26

gaagaggcaa gacgcttgta c

21

<210> 27

<211> 21

<212> DNA

<213> Homo sapiens

<400> 27

gtacaagcgt cttgcctctt c 21

<210> 28
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 28
 gagtttgagc agatgttta 19

<210> 29
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<221> misc_feature
 <222> 3, 9, 15
 <223> n = A,T,C or G

<400> 29
 ggnaargcnc ayccncargc 20

<210> 30
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<221> misc_feature
 <222> 3, 6, 21
 <223> n = A,T,C or G

<400> 30
 atngcnggrt aytgytgdat ntc 23

<210> 31
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide

<400> 31
 grgayttraw bgabgchyam gawtgg 26

<210> 32
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 32

caagcbtggg aymtymtyta ytatmaygtb ttcag

35

<210> 33

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 33

gayybgartt ggctgtbcch gg

22

<210> 34

<211> 327

<212> DNA

<213> Homo sapiens

<400> 34

atgtccgtac	aagtagaaac	catctcccca	ggagacgggc	gcaccttccc	caagcgcggc	60
cagacctgcg	tggtgcacta	caccgggatg	cttgaagatg	gaaagaaatt	tgattcctcc	120
cgtgaccgta	acaagccctt	taagtttatg	ctaggcaagc	aggaggtgat	ccgaggctgg	180
gaagaagggg	ttgccagat	gagtgtgggt	cagcgtgcc	aactgactat	atctccagat	240
tatgcctatg	gtgccactgg	gcaccaggc	atcatccac	cacatgccac	tctcgtcttc	300
gatgtggagc	ttctaaaact	ggaatga				327

<210> 35

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 35

gagatctgga attcggatcc tgcgagagatc t

31